Intraspecific variation detected in West African Soft-furred Mice, *Praomys rostratus*, through molecular phylogenetics (*Cytb*) and morphology

Research Thesis

Presented in partial fulfillment of the requirements for graduation *with research distinction* in the undergraduate colleges of The Ohio State University.

by

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Abstract

The Upper Guinea Forest ranges across six countries in West Africa and has unique biodiversity including many endemic species. Among these endemic species is the West African Soft-furred Mouse, *Praomys rostratus*. *Praomys rostratus* is nearly indistinguishable morphologically from its sister species, *P. tullbergi*, and is often misidentified in the field. I used phylogenetic and morphological analyses to test for intraspecific variation within *P. rostratus* across three regions: central Sierra Leone, southeastern Guinea, and western Côte d'Ivoire. Cytochrome b sequences (n=117) were analyzed using a coalescent Bayesian Skyline model to construct a phylogenetic tree depicting relative divergence times. With the same samples, I evaluated Kimura 2-parameter distances to test for species-level distances. I also used five field measurements to test for sexual dimorphism and morphological variation in 120 samples. The six measurements include weight (g), total body length (mm), body length (mm), tail length (mm), hind tarsus length (mm), and ear length (mm). A MANOVA and ANOVA were used to analyze these data. My genetic results showed that *P. rostratus* splits into two separate clades based on location: Sierra Leone and Guinea/Côte d'Ivoire. My morphological results showed that Côte d'Ivoire samples are significantly larger than samples from Sierra Leone and Guinea. From these results I conclude that there is intraspecific variation present in the phylogeny and morphology of *P. rostratus* that correlates with its geographical distribution. However, the results from the two approaches used do not agree.

Introduction

The Upper Guinea Forest ranges across six West African countries (Conservation International 1999). This forest is home to a minimum of 41 biodiversity hotspots across Sierra Leone, Guinea, Liberia, Côte d'Ivoire, and Togo (Conservation International 1999). Sierra Leone houses lowland forest, forest-savanna, and semi-deciduous forest (Conservation International 1999; Decher et al. 2010). Guinea consists of a transition zone of mosaic forest and savanna (Conservation International 1999). Dense rain forest and contiguous forest can be found at the border of Liberia and Côte d'Ivoire (Conservation International 1999).

Sierra Leone, Guinea, and Côte d'Ivoire are all considered biodiversity hotspots for mammals, including rodents (Conservation International 1999). Rodents have short generation times, limited dispersal, and are sensitive to habitats which makes them ideal for studying intraspecific variation (Nicolas et al. 2008; Chavel et al. 2017).

Our study examines intraspecific variation in the West African Soft-furred Mouse, *Praomys rostratus,* (Rodentia, Murinae). It is a red-brown, nocturnal rodent that dwells in western Upper Guinean Forests (Nicolas et al. 2005; Norris 2006; Denys et al. 2017). This generalist rodent belongs to an omnivorous complex, and it ranges from Senegal through Côte d'Ivoire (Nicolas et al. 2005; Michaux et al. 2007; Denys et al 2017). *Praomys rostratus* is predominantly found during collection, as its habitat includes (1) stream in derived savanna, (2) wooded savanna, (3) forest edge, (4) forest clearing, (5) stream in forest, (6) forest, and (7) gallery forest (Norris 2006).

Phylogenetics and taxonomy for the genus *Praomys* have been heavily researched and debated. Low levels of morphological variation between species and a large number of sibling species continue to vex attempts to reconstruct the evolutionary history of the group (Lecompte

et al. 2002a, 2005; Akpatou et al. 2007; Nicolas et al. 2012). In the past two decades alone, many studies on *Praomys* have been conducted to investigate its evolutionary radiations, phylogenetic implications, adaptive convergences, taxonomic classification, and general systematics (Lecompte 2002a, 2002b, 2005, 2008; Nicolas et al. 2005, 2008, 2012; Akpatou 2007).

Praomys rostratus (Miller, 1900), my focal organism, and its sister species *P. tullbergi* (Thomas, 1894) are genetically different (Nicolas et al. 2008), yet their extremely similar cranial morphology continues to lead to misidentifications as explained in a review by Akpatou et al. (2007). This difficulty with identification was experienced firsthand by R. W. Norris who collected *P. rostratus* in Sierra Leone and Guinea. After working in the field with the species in Sierra Leone and Guinea, Norris determined that the *Praomys* he collected in Sierra Leone seemed smaller than those from Guinea. In Sierra Leone they were often initially confused with a smaller rodent, *Hylomyscus*. Additionally, when Norris was in Déré and Diécké, Guinea (Norris 2006), he often initially confused *Praomys* with a larger rodent, *Malacomys*. The Sierra Leone samples were identified as *P. tullbergi* (Decher et al. 2010), whereas all samples from Guinea were identified as *P. rostratus* (Norris 2006; Decher et al. 2009). Later genetic analysis (Nicolas et al. 2008) showed that all specimens from both locations were *P. rostratus* but suggested that samples from Sierra Leone were distinct. Based on this and other observations, Norris predicted they represented two separate species. Experiences in the field and genetic results from Nicolas et al. (2008) brought about my thesis project.

My thesis uses field measurements and sequenced cytochrome b (*Cytb*) genes (Nicolas et al. 2008) to study intraspecific variation in *P. rostratus* from three regions: central Sierra Leone, southeastern Guinea, and another well-sampled region in western Côte d'Ivoire (Fig. 1). Nicolas et al. (2008) used a simple Bayesian phylogenetic method, but coalescent-based models are

arguably more appropriate for intraspecific studies (Drummond et al. 2005). My research investigates the relationship between geographic distribution, phylogeny, and morphology of *P. rostratus*. This study will address two questions: 1) Is phylogenetic variation present on a molecular level between or across the geographic range of this species? 2) Are regional morphological variations present between or across the geographic range of this species?

Materials and Methods:

Molecular Phylogenetics.— Samples used for this study (Appendix A) were obtained from three locations: Sierra Leone (SL), Guinea (Gu), and Côte d'Ivoire (IC), West Africa. *Praomys rostratus* Cytochrome b (*Cytb*) samples (n=117) from Nicolas et al. (2008) were downloaded for my analysis from GenBank. Sierra Leone (n=15), Guinea (n = 50), and Côte d'Ivoire samples (n = 52) in Figure 1 are illustrated by red, yellow, and blue dots respectively. Two samples of *P. tullbergi* were also obtained from GenBank and used as an outgroup for the entirety of the project. A nexus file was created these 117 samples and were aligned by eye. The correct model of evolution was selected using JModeltest 2.1.7 (Darriba et al. 2012), which yielded a GTR substitution model with Gamma site heterogeneity. The BEAST analysis was set up using a lognormal uncorrelated relaxed clock and a Coalescent Bayesian Skyline tree prior with 5 groups and a random starting tree. There are no fossil calibrations available for *P. rostratus*. This is because *P. rostratus* lives in moist West African rainforest where fossil preservation is poor. To compensate for this, we set our priors to an original divergence time between *P. rostratus* and *P. tullbergi* to a mean of 1.00 with a standard deviation of 0.001. Therefore, all divergence times on the tree are expressed as a proportion of the time when *P. rostratus* diverged from *P. tullbergi*. The MCMC consisted of a chain length of 100,000,000

generations, with a tree sampled every 10,000 generations. A burn in of 10,000 generations was also applied. This file was uploaded and run on the Cyberinfrastructure for Phylogenetic Research Science Gateway V.3.3 (CIPRES – Miller et al. 2010). I then took the output from CIPRES and visualized it in Tracer v1.6 (Rambaut et al. 2014). All ESS values were over one hundred. I used FigTree v.1.4.3 to create Figure 2.

All pairwise Kimura 2-parameter distances between samples were determined using PAUP* 4.0a (Swofford 2002). To do this I first set our distance settings to DNA/RNA distance and then used the Kimura 2-parameter (K2P) option. PAUP* produced a distance matrix of samples from SL, Gu, and IC to create Figure 3. According to Baker and Bradley, (2006) the lower cutoff for species-level distances in rodents is typically a K2P value of 0.02 and the upper cut off is typically 0.10. This cutoff is applied to all of my genetic results and illustrated by a black line in Figure 3.

Morphology.— The *P. rostratus* samples (n=120) used for this study were collected in the Upper Guinea Forest in West Africa. Sierra Leone (n=11), Guinea (n=77), and Côte d'Ivoire samples (n=32) in Figure 1 are illustrated by red, yellow, and blue dots outlined in black respectively. Norris, J. Decher, and colleagues collected samples from sites in Sierra Leone (Decher et al. 2010) and Guinea (Norris 2006; Decher et al. 2010). Samples from Côte d'Ivoire were collected during expeditions led by the Field Museum of Natural History. Measurements for weight (g), total body length "TBL" (mm), tail length "TL" (mm), hind tarsus length "HL" (mm), and ear length "EL" (mm) were collected in the field. To better standardize measurements, I calculated the body length "BL" (mm) by subtracting the TL from the TBL.

Morphological statistics were calculated using both JMP Pro 14.0.0 and R (version 3.6.0). The program R (version 3.6.0) was used to calculate the mean and standard deviation for

the measurements of weight, TBL, BL, TL, HL, and EL in all three locations. JMP was then used to run a Principle Component Analysis (PCA) to test for any correlation between the six measurements. Then JMP was used to cross analyze sex and location in order to test for an interaction. Next, JMP was used to run an ANOVA with a best fit model to test for sexual dimorphism. The y-value was set to use PC1 and the x-values included sex, location, and the interaction between sex and location. Another ANOVA was run in JMP to test for variation in measurements across location: SL, Gu, and IC. Again, our y-value was PC1 and our x-value was sex, location, and the interaction between sex and location. A MANOVA was run in JMP with the sum option and conducted with post hoc pairwise contrasts to test the six variables among location subsets including "SL vs Gu," "SL vs IC," and "Gu vs IC."

Results

Molecular Phylogenetics.— *Praomys rostratus* was recovered as monophyletic with a Bayesian posterior probability (BPP) of 0.93. Two major clades of *P. rostratus* were recovered, both with a BPP of 1.00. The first clade consisted of all Sierra Leone samples except one. The second clade is composed of all Guinea and Côte d'Ivoire samples, along with the one individual from Sierra Leone. The divergence time of the two clades was 0.52 (95% Highest Posterior Density (HPD) = 0.84 to 0.27) (Fig. 2). The node age of the SL clade is 0.11 (95% HPD = 0.23 to 0.03), and the node age of the Gu/IC clade is 0.24 (95% HPD 0.40 to 0.11).

The results from the K2P analysis match what we see in the phylogenetic tree. There are three peaks present in Figure 3, which correspond to within clade comparisons (left), between clade comparisons (middle), and between species comparisons (right). As expected, the right peak consists of only "*P. rostratus* vs *P. tullbergi*" samples (K2P range 0.046 to 0.064). This

distance is to the right of the Baker and Bradley (2006) lower cut off point for species level distances (=0.02). The middle peak primarily consists of two groups: SL vs Gu (K2P range 0.004 to 0.035), and SL vs IC (K2P range 0.006 to 0.036). All of these samples were placed to the right of the Baker and Bradley (2006) lower cut off point. This peak also includes a "SL vs SL" section (K2P range 0.021 to 0.024). The peak on the left consists of groups to the left of Baker and Bradley (2006) lower cut off point. These are SL vs SL (K2P range from 0 to 0.008), Gu vs Gu (K2P range 0 to 0.017), IC vs IC (K2P range 0 to 0.02), and Gu vs IC (K2P range 0.004 to 0.023). The one sample from SL that can be found in the Gu/IC clade from Figure 2 is why we see a "SL vs SL" section in the middle peak (K2P range 0.021 to 0.024).

Morphology.— Table 1 shows the mean and standard deviation for the six measurements taken from SL, Gu, and IC. Our PCA resulted in a high correlation between all six measurements Table 2. PC1 resulted in an eigenvalue of 3.5777. Out of all four eigenvalues, this was the only value to reach above a score of 2.0. The eigenvectors for PC1 are TBL= 0.51278, BL= 0.47488, TL= 0.48108, HL= 0.39677, and EL= 0.35026.

Sexual dimorphism was not detected in the 120 samples (males n=78, females n=42) for the six measurements ($F_{5,107} = 3.4694$, $p < 0.0060$). Likewise, a difference was not present for the individual effects of sex ($F_{5,107} = 0.8932$, $p < 0.3467$) or the interaction between sex and location ($F_{5,107} = 1.2656$, $p < 0.2862$). There was a difference due to location ($F_{5,107} = 4.2375$, $p < 0.0169$).

Significant variation was detected in morphology due to location. The MANOVA test recover a significant difference between SL and IC ($F_{1,107} = 5.3060$, $p < 0.0232$), as well as Gu and IC ($F_{1,107} = 7.4337$, $p < 0.0075$). The MANOVA test did not recovered a significant difference between SL and Gu ($F_{1,107} = 0.4589$, $p < 0.4996$). This is more easily viewed in Table

1, which shows an increase in mean sizes from northwest (SL) to southeast (IC) for the three locations across all five variables. From the MAVOVA, I conclude that Côte d'Ivoire samples are significantly larger than Sierra Leone and Guinea.

Discussion

The results from my study are significant, yet different in nature. Intraspecific variation is present for both phylogeny and morphology in correlation with *P. rostratus* geographic distribution. Sierra Leone samples are phylogenetically different from Gu and IC, while Côte d'Ivoire samples are morphologically different from SL and Gu samples.

Praomys rostratus samples from Sierra Leone are monophyletic, except for one sample that will be discussed later. These results match Nicolas et al. (2008), but with stronger support using a different phylogenetic approach. The second clade produced by our tree contains Guinea/Côte d'Ivoire samples. The two clades (SL and Gu/IC) have a greater K2P than the Baker and Bradley (2006) lower cut off point for species-level distances. The one samples from SL that falls into the Gu/IC clade also pushes a section of the SL vs SL samples to the right of the Baker and Bradley (2006) lower cut off point for species-level distances. From this, I can suggest that there may be a separation between the SL clade and Gu/IC clade, distinct enough to be a species or subspecies.

The clade I recovered for Sierra Leone is unique to *P. rostratus*, as these results do not parallel with results in *Dephomys, Typomys,* and *Malacomys* in the same regions (Bohoussou et al. 2015; Bauer 2019). Bauer (2019) suggested that this is due local extinction in Sierra Leone during an aridity event and subsequent migration from Guinea for *Dephomys, Typomys,* and *Malacomys.* He proposed that because *P. rostratus* is a generalist, it could have persisted in poor

quality forest in Sierra Leone during aridity events. These animals may be the ancestors of my Sierra Leone clade. After this period of aridity ended, fragmented forest expanded, allowing for gene flow. This can explain the mitochondrial introgression that may be the cause of the one Sierra Leone sample that is in the wrong clade.

The results from my morphological data suggest the presence of intraspecific variation in *P. rostratus*. However, the morphological results are focused on IC, which is opposite of the phylogenetic results that show SL as unique. I propose that these results might be due to a latitudinal reversal of Bergmann's Rule. Bergmann's Rule states that animals tend to be larger in cooler environments and smaller in warmer environments (Ashton et al. 2000; Nwaogu et al. 2018). However, one study conducted in West Africa on the Common Bulbul, *Pycnonotus barbatus*, suggests that in the tropics Bergmann's rule can be flipped (Nwaogu et al. 2018). Animals in the dense forests at low latitudes (IC) in Upper Guinea are likely experiencing less heat stress than those in the drier and open habitat at higher latitudes (SL). I suggest that same pattern may be present in the *P. rostratus* in my data set.

There are two confounding variables that I was unable to control during this project. These confounds could have skewed my results. First, I do not know if there were juveniles present in the SL and Gu samples. Because I did not observe physical skull samples from the Smithsonian for SL and Gu, I was unable to identify juveniles from adults. Although I did know which IC samples were juveniles, I did not remove them from my sample because I did not want to introduce bias into the project. Secondly, my sample sizes are not ideal. I had an almost equal number of samples from Guinea (n= 50, 77) and Côte d'Ivoire (n = 52, 32). On the contrary, I only had 15 and 11 samples from Sierra Leone. Larger sample sizes for Sierra Leone are needed

to capture if the patterns we see are consistent or not. Overall, I would need to eliminate juveniles and increase sample size to minimize potential error in these results.

In conclusion, geographic distribution is correlated with intraspecific variation present in phylogeny and morphology of *P. rostratus*. The genetic data suggest that there might be a distinct subspecies of *P. rostratus* in Sierra Leone, but morphological data suggest that it is Côte d'Ivoire that is morphologically distinct. The morphological differences may be due to a size gradient related to Bergmann's Rule. Further research investigating *P. rostratus* without juveniles and an increased sample size needs to be conducted to fully understand what type of intraspecific variation is occurring in West Africa.

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Figure Legend

Figure 1 – Map of Africa (left) with a focus on the Upper Guinea region (right). Samples for phylogenetic analyses were collected from sites in Sierra Leone (yellow), Guinea (red), and Côte d'Ivoire (blue). Samples were collected in the same regions for morphological analysis and are illustrated by a black outlined circle.

Figure 2 – Bayesian skyline phylogenetic tree showing divergence time of *Praomys* samples (Appendix A) from Sierra Leone, Guinea, and Côte d'Ivoire. Clades have been collapsed if they contain a single location: Sierra Leone, Guinea, and Côte d'Ivoire. The outgroup clade is labeled "*P. tullbergi"* and represents two samples from a sister taxon. These samples are from Ghana and Coté d'Ivoire. Values at the nodes represent Bayesian Posterior Probability. Bars represent age range produced from 95% Highest Posterior Density.

Figure 3 – Stacked histogram displaying each of the seven categories and how their frequency compares on a Kimura 2 Parameter Distance scale. Brown represents *Praomys tullbergi* vs *Praomys rostratus*. Red represents Sierra Leone vs Sierra Leone (SL vs SL). Yellow represents Guinea vs Guinea (Gu vs Gu). Blue represents Côte d'Ivoire vs Côte d'Ivoire (IC vs IC). Orange represents Sierra Leone vs Guinea (SL vs Gu). Purple represents Sierra Leone vs Côte d'Ivoire (SL vs IC). Green represents Guinea vs Côte d'Ivoire (Gu vs IC). The black line represents the lower cutoff of 0.02 for species-level distances in rodents, according to Baker and Bradley (2006). The upper cutoff for sister species is 0.10 and is not shown.

Figure 1


AFRICA
Area of detail
ATLANTIC OCEAN
GUINEA BISSAU
GUINEA
MALI
SIERRA LEONE
CÔTE D'IVOIRE
LIBERIA
N
500 km

Figure 2

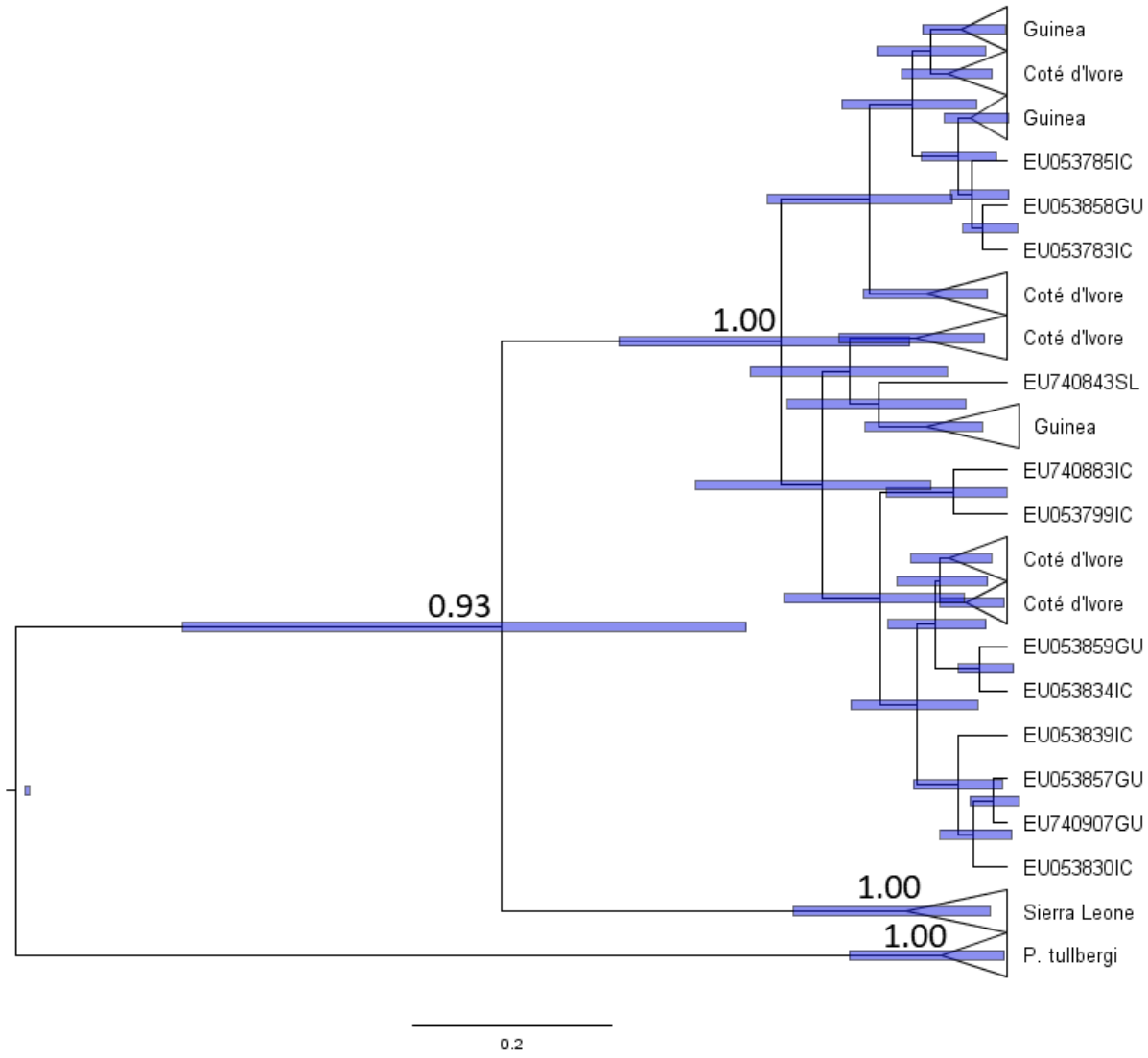
Guinea
Coté d'Ivore
Guinea
EU053785IC
EU053858GU
EU053783IC
Coté d'Ivore
Coté d'Ivore
EU740843SL
Guinea
EU740883IC
EU053799IC
Coté d'Ivore
Coté d'Ivore
EU053859GU
EU053834IC
EU053839IC
EU053857GU
EU740907GU
EU053830IC
Sierra Leone
P. tullbergi
1.00
0.93
1.00
1.00
0.2

Figure 3

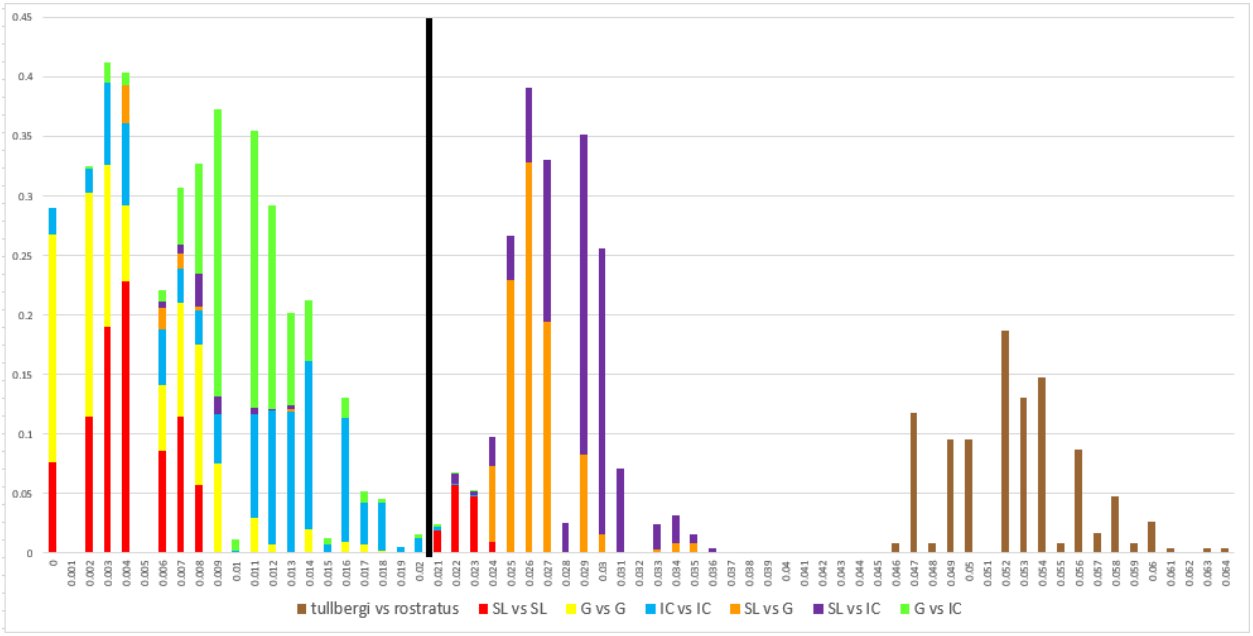
0.45
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
tullbergi vs rostratus
SL vs SL
G vs G
IC vs IC
SL vs G
SL vs IC
G vs IC

Table 1 – There were 120 *P. rostratus* samples used for this study (Sierra Leone = 11, Guinea = 77, Côte d'Ivoire = 32). The mean and the standard deviation were calculated in R (Version 3.6.0) for five field measurements: weight, body length, tail length, hind tarsus length, and ear length.

	Sierra Leone	**Guinea**	**Côte d'Ivoire**
Weight (g)	38.38 +/- 18.55	42.65 +/- 12.15	49.16 +/-12.93
Body Length (mm)	111.64 +/- 19.77	115.82 +/- 11.85	129.81 +/- 13.92
Tail Length (mm)	133.45 +/- 26.42	138.18 +/- 19.74	145.69 +/- 13.38
Hind Tarsus (mm)	24.82 +/- 2.60	24.82 +/- 1.76	25.91 +/- 1.38
Ear Length (mm)	17.73 +/- 1.79	18.53 +/- 2.13	18.72 +/- 1.42

Table 2 – There were 120 *P. rostratus* samples used for this study (Sierra Leone = 11, Guinea = 77, Côte d'Ivoire = 32). Five measurements (total body length (mm), tail length (mm), hind tarsus length (mm), and ear length (mm)) were collected in the field at three localities. Body length was calculated by subtracting the tail length from the total body length. A PCA was conducted to test for correlation among the 5 measurements. The following pairwise comparisons were generated by this PCA.

	Total Body	Body	Tail	Hind Tarsus	Ear
Total Body	1.00	0.9117	0.9492	0.6235	0.5276
Body	0.9117	1.00	0.7361	0.6003	0.4690
Tail	0.9492	0.7361	1.00	0.5674	0.5100
Hind Tarsus	0.6235	0.6003	0.5674	1.00	0.4139
Ear	0.5276	0.4690	0.5100	0.4139	1.00

Appendix A. Locality and GenBank numbers for *Praomys* samples used in this study.

Species	**GenBank #**	**Locality**	**Country**
P. tullbergi	EU053715	Mamang River	Ghana
P. tullbergi	EU053737	Azagny National Park	Côté d'Ivoire
P. rostratus	EU740841	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740842	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740843	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740844	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740845	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740846	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740847	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740848	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740849	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740850	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740851	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740852	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740853	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740854	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740855	Seli River, Bumbuna	Sierra Leone
P. rostratus	EU740900	Bhoita	Guinea
P. rostratus	EU740901	Bhoita	Guinea
P. rostratus	EU740902	Bamakama	Guinea
P. rostratus	EU053857	Diécké	Guinea
P. rostratus	EU740907	Diécké	Guinea
P. rostratus	EU053856	Diécké	Guinea
P. rostratus	EU053858	Diécké	Guinea
P. rostratus	EU053859	Diécké	Guinea
P. rostratus	EU740908	Franfina	Guinea

P. rostratus	EU740706	Franfina	Guinea
P. rostratus	EU740707	Franfina	Guinea
P. rostratus	EU740708	Franfina	Guinea
P. rostratus	EU740909	Franfina	Guinea
P. rostratus	EU740910	Franfina	Guinea
P. rostratus	EU740709	Franfina	Guinea
P. rostratus	EU740755	Maikou	Guinea
P. rostratus	EU740756	Maikou	Guinea
P. rostratus	EU740757	Maikou	Guinea
P. rostratus	EU740934	Maikou	Guinea
P. rostratus	EU740935	Maikou	Guinea
P. rostratus	EU740936	Maikou	Guinea
P. rostratus	EU523544	Nimba Mount	Guinea
P. rostratus	EU053860	Nimba Mount	Guinea
P. rostratus	EU053841	Ziama forest, Balassou	Guinea
P. rostratus	EU053849	Ziama forest, Malwéta	Guinea
P. rostratus	EU053850	Ziama forest, Malwéta	Guinea
P. rostratus	EU053842	Ziama forest, Balassou	Guinea
P. rostratus	EU053843	Ziama forest, Balassou	Guinea
P. rostratus	EU053851	Ziama forest, Balassou	Guinea
P. rostratus	EU053852	Ziama forest, Malwéta	Guinea
P. rostratus	EU053844	Ziama forest, Malwéta	Guinea
P. rostratus	EU053845	Ziama forest, Malwéta	Guinea
P. rostratus	EU053846	Ziama forest, Balassou	Guinea
P. rostratus	EU740937	Ziama forest, Malwéta	Guinea
P. rostratus	EU053853	Ziama forest, Malwéta	Guinea
P. rostratus	EU053854	Ziama forest, Malwéta	Guinea
P. rostratus	EU053847	Ziama forest, Balassou	Guinea

P. rostratus	EU740938	Ziama forest, Balassou	Guinea
P. rostratus	EU740939	Ziama forest, Malwéta	Guinea
P. rostratus	EU740940	Ziama forest, Balassou	Guinea
P. rostratus	EU740941	Ziama forest, Balassou	Guinea
P. rostratus	EU053855	Ziama forest, Malwéta	Guinea
P. rostratus	EU053848	Ziama forest, Malwéta	Guinea
P. rostratus	EU740946	Sangassou	Guinea
P. rostratus	EU740947	Sangassou	Guinea
P. rostratus	EU740948	Sangassou	Guinea
P. rostratus	EU740949	Sangassou	Guinea
P. rostratus	EU740950	Sangassou	Guinea
P. rostratus	EU740951	Sangassou	Guinea
P. rostratus	EU740952	Sangassou	Guinea
P. rostratus	EU053780	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053782	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053783	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU740883	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053781	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU740884	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053784	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU740885	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053799	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053791	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053785	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053787	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053789	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053788	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU0523545	Djidoubaye Forest	Côté d'Ivoire

P. rostratus	EU053790	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053786	Djidoubaye Forest	Côté d'Ivoire
P. rostratus	EU053793	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU053794	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU053795	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU740887	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU053796	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU740888	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU0523546	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU053792	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU740889	Gaourou Forest	Côté d'Ivoire
P. rostratus	EU053801	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053802	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053810	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053803	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU740890	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053804	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053805	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053806	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU740891	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053811	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053807	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053808	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053809	Monogaga Forest	Côté d'Ivoire
P. rostratus	EU053836	Taï National Park	Côté d'Ivoire
P. rostratus	EU053829	Taï National Park	Côté d'Ivoire
P. rostratus	EU053830	Taï National Park	Côté d'Ivoire
P. rostratus	EU053837	Taï National Park	Côté d'Ivoire

P. rostratus	EU053838	Taï National Park	Côté d'Ivoire
P. rostratus	EU053831	Taï National Park	Côté d'Ivoire
P. rostratus	EU053832	Taï National Park	Côté d'Ivoire
P. rostratus	EU740942	Taï National Park	Côté d'Ivoire
P. rostratus	EU053839	Taï National Park	Côté d'Ivoire
P. rostratus	EU053840	Taï National Park	Côté d'Ivoire
P. rostratus	EU053833	Taï National Park	Côté d'Ivoire
P. rostratus	EU740943	Taï National Park	Côté d'Ivoire
P. rostratus	EU053834	Taï National Park	Côté d'Ivoire